

FIGURE 1

full length pmt cDNA

[illegible]

FIGURE 2A

06-03-2017

full length pmt cDNA

+1	Trp	Lys	Ser	Phe	Phe	His	Trp	Ser	Leu	Met	Ala	Leu	Ile	Leu	Phe	Leu	Val
751	TGGAAGAGTT	TCTTTCATTG	GTCGCTGATG	GCCCTCATAC	TATTTCTGGT	ACCTTCTCAA	AGAAAGTAAC	CAGCGACTAC	CGGGAGTATG	ATAAAGACCA							
+1	Val	Pro	Val	Val	Val	Ile	Asp	Ser	Tyr	Tyr	Tyr	Gly	Lys	Leu	Val	Ile	Ala
801	GCCTGTGGTG	GTCATTGACA	GCTACTATTA	TGGGAAGTTG	GTGATTGCAC	CGGACACCAC	CAGTAACTGT	CGATGATAAT	ACCCTTCAAC	CACTAACGTG							
+1	Pro	Leu	Asn	Ile	Val	Leu	Tyr	Asn	Val	Phe	Thr	Pro	His	Gly	Pro	Asp	Leu
851	CACTCAACAT	TGTTTTGTAT	AATGTCTTTA	CTCCTCATGG	ACCTGATCTT	GTGAGTTGTA	ACAAAACATA	TTACAGAAAT	GAGGAGTACC	TGGACTAGAA							
+1	Tyr	Gly	Thr	Glu	Pro	Trp	Tyr	Phe	Tyr	Leu	Ile	Asn	Gly	Phe	Leu	Asn	Phe
901	TATGGTACAG	AACCCTGGTA	TTTCTATTTA	ATTAATGGAT	TTCTGAATTT	ATACCATGTC	TTGGGACCAT	AAAGATAAAT	TAATTACCTA	AAGACTTAA							
+1	Phe	Asn	Val	Ala	Phe	Ala	Leu	Ala	Leu	Leu	Val	Leu	Pro	Leu	Thr	Ser	Leu
951	CAATGTAGCC	TTTGCTTTGG	CTCTCCTAGT	CCTACCACTG	ACTTCTCTTA	GTTACATCGG	AAACGAAACC	GAGAGGATCA	GGATGGTGAC	TGAAGAGAAT							
+1	Met	Glu	Tyr	Leu	Leu	Gln	Arg	Phe	His	Val	Gln	Asn	Leu	Gly	His	Pro	Tyr
1001	TGGAATACCT	GCTGCAGAGA	TTTCATGTTC	AGAATTTAGG	CCACCCGTAT	ACCTTATGGA	CGACGTCTCT	AAAGTACAAG	TCTTAAATCC	GGTGGGCATA							
+1	Trp	Leu	Thr	Leu	Ala	Pro	Met	Tyr	Ile	Trp	Phe	Ile	Ile	Phe	Phe	Ile	Gln
1051	TGGCTTACCT	TGGCTCCAAT	GTATATTTGG	TTTATAATTT	TCTTCATCCA	ACCGAATGGA	ACCGAGGTTA	CATATAAACC	AAATATTAAA	AGAAGTAGGT							
+1	Gln	Pro	His	Lys	Glu	Glu	Arg	Phe	Leu	Phe	Pro	Val	Tyr	Pro	Leu	Ile	Cys
1101	GCCTCACAAA	GAGGAGAGAT	TTCTTTTCCC	TGTGTATCCA	CTTATATGTC	CGGAGTGTTT	CTCCTCTCTA	AAGAAAAGGG	ACACATAGGT	GAATATACAG							
+1	Leu	Cys	Gly	Ala	Val	Ala	Leu	Ser	Ala	Leu	Gln	Lys	Cys	Tyr	His	Phe	Val
1151	TCTGTGGCGC	TGTGGCTCTC	TCTGCACTTC	AGAAATGTTA	CCACTTTGTG	AGACACCGCG	ACACCGAGAG	AGACGTGAAG	TCTTTACAAT	GGTGAAACAC							
+1	Phe	Gln	Arg	Tyr	Arg	Leu	Glu	His	Tyr	Thr	Val	Thr	Ser	Asn	Trp	Leu	Ala
1201	TTTCAACGAT	ATCGCCTGGA	GCACTATACT	GTGACATCGA	ATTGGCTGGC	AAAGTTGCTA	TAGCGGACCT	CGTGATATGA	CAC TGTAGCT	TAACCGACCG							
+1	Ala	Leu	Gly	Thr	Val	Phe	Leu	Phe	Gly	Leu	Leu	Ser	Phe	Ser	Arg	Ser	Val
1251	ATTAGGAAC	GTCTTCCTGT	TTGGGCTCTT	GTCATTTTCT	CGCTCTGTGG	TAATCCTTGA	CAGAAGGACA	AACCCGAGAA	CAGTAAAGA	GCGAGACACC							
+1	Ala	Leu	Phe	Arg	Gly	Tyr	His	Gly	Pro	Leu	Asp	Leu	Tyr	Pro	Glu	Phe	Tyr
1301	CACTGTTTCA	AGGATATCAC	GGGCCCCCTG	ATTTGTATCC	AGAATTTTAC	GTGACAAGTC	TCCTATAGTG	CCCGGGGAAC	TAAACATAGG	TCTTAAAATG							
+1	Arg	Ile	Ala	Thr	Asp	Pro	Thr	Ile	His	Thr	Val	Pro	Glu	Gly	Arg	Pro	Val
1351	CGAATTGCTA	CAGACCCAAC	CATCCACACT	GTCCCAGAAG	GCAGACCTGT	GCTTAACGAT	GTCTGGGTTG	GTAGGTGTGA	CAGGGTCTTC	CGTCTGGACA							
+1	Val	Asn	Val	Cys	Val	Gly	Lys	Glu	Trp	Tyr	Arg	Phe	Pro	Ser	Ser	Phe	Leu
1401	GAATGTCTGT	GTGGGAAAAG	AGTGGTATCG	ATTTCCAGC	AGCTTCCTTC	CTTACAGACA	CACCTTTTTC	TCACCATAGC	TAAAGGGTCG	TCGAAGGAAG							
+1	Leu	Pro	Asp	Asn	Trp	Gln	Leu	Gln	Phe	Ile	Pro	Ser	Glu	Phe	Arg	Gly	Gln
1451	TTCCTGACAA	TTGGCAGCTT	CAGTTCATTC	CATCAGAGTT	CAGAGGTCAG	AAGGACTGTT	AACCGTCGAA	GTCAAGTAAG	GTAGTCTCAA	GTCTCCAGTC							

FIGURE 2A

DEPARTMENT OF THE ARMY

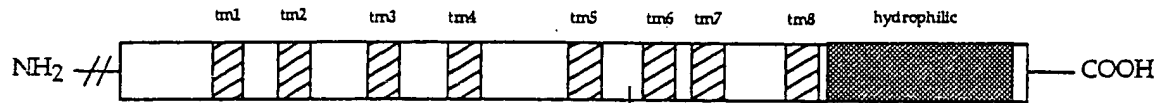
069927Z JUL 80

Translation of full length pmt cDNA

1	MASRGARQRL	KGSGASSGDT	APAADKLREL	LGSREAGGAE	HRTLSGNKA
51	GQVWAPEGST	AFKCLLSARL	CAALLSNISD	CDETFNYWEP	THYLIYGEGE
101	QTWEYSPAYA	IRSYAYLLLH	AWPAAFHARI	LQTNKILVEY	FLRCLLAEVS
151	CICELYFYKA	VCKKFGLHVS	RMMLAFLVLS	TGMFCSSSAF	LPSSFCMYTT
201	LIAMTGWYMD	KTSIAVLGVA	AGAILGWPF	AALGLPIAFD	LLVMKHRWKS
251	FFHWSLMALI	LFLVPVVVID	SYYYGKLVIA	PLNIVLYNVF	TPHGPDLYGT
301	EPWYFYLING	FLNFNVAFAL	ALLVLPLTSL	MEYLLQREHV	QNLGHPYWLT
351	LAPMYIWFII	FFIQPHKEER	FLFPVYPLIC	LCGAVALSAL	QKCYHFEVQR
401	YRLEHYTVTS	NWLALGTVFL	FGLLSFSRSV	ALFRGYHGPL	DLYPEFYRIA
451	TDPTIHTVPE	GRPVNVCVGK	EWYRFPSSFL	LPDNWQLQFI	PSEFRGQLPK
501	PFAEGPLATR	IVPTDMNDQN	LEEPSRYIDI	SKCHYLVDLD	TMRETPREPK
551	YSSNKEEWIS	LAYRPFLDAS	RSSKLLRAFY	VPFLSDQYTV	YVNYTILKPR
601	KAKQIRKKSG	G			

Schematic of Fusion Open Reading Frame

putative Mannose Transferase



CGTACAATGTGAAGAAAGTCCTTGATCCCTT 31
CGCCTTCGCCATAATGGCAGGGGCATCCAGTGGTTCAAGGTTACAATAAGCTGTGATCGTGCCACTGCATTCTACCTGGG 112

1 M T E W D P V P Q S E T L S Q K K K L C K S K E T T S
AIGACAGAGTGGGACCCTGTGCCACAGAGTGAGACCCTGTCTCAAAAAAAAAAACTATGTAAATCCAAGGAGACGACTTCA 193
28 P V L Y L S K F W K V D G G F T Q N F N L S R T E F C
CCTGTATTGTACCTCTCCAAGTTCTGGAAAGTCGATGGAGGGTTTACTCAGAACTTCAATCTATCCAGAACTGAGTTTGT 274

Fusion Partner

55 L W C V P
TTATGGTGTGTGCCAG 290
CTGCAGAGATTTCATGTTTCAGAATTTAGGCCACCCGATTGGCTTACCTTGGCTCCAATGTATATTTGGTTTATAATTTTC 355
V Q N L G H P Y W L T L A P M Y I W F I I F

Exon 7* Exon 8*

TTCATCCAGCCTCACAAAGAGGAGAGATTTCTTTTCCCTGTGTATCCACTTATATGTCTCTGTGGCGCTGTGGCTCTCTCT 436
82 F I Q P H K E E R F L F P V Y P L I C L C G A V A L S
GCACTTCAGAAATGTTACCACTTTGTGTTTCAACGATATCGCCTGGAGCACTATACTGTGACATCGAATTGGCTGGCATT 517
109 A L Q K C Y H F V F Q R Y R L E H Y T V T S N W L A L
GGAAGTGTCTTCTGTTTGGGCTCTTGTCTGCTCTGTGGCACTGTTTCAGAGGATATCACGGGCCCCCTTGATTG 598
136 G T V F L F G L L S F S R S V A L F R G Y H G P L D L
TATCCAGAATTTTACCGAATTGCTACAGACCCAACCATCCACACTGTCCAGAAGGCAGACCTGTGAATGTCTGTGTGGGA 679
163 Y P E F Y R I A T D P T I H T V P E G R P V N V C V G
AAAGAGTGGTATCGATTTCCAGCAGCTTCTTCTCTGACAATTGGCAGCTTCAGTTCAATCCATCAGAGTTTCAGAGGT 760
190 K E W Y R F P S S F L L P D N W Q L Q F I P S E F R G
CAGTTACCAAAACCTTTTGCAGAAGGACCTCTGGCCACCCGGATTGTTCTACTGACATGAATGACCAGAATCAGAAGAGC 841
217 Q L P K P F A E G P L A T R I V P T D M N D Q N Q K S
CATCCAGATATATTGATATCAGTAAATGCCATTATTAG 880
243 H P D I L I S V N A I I .

Partner - putative Mannose Transferase fusion

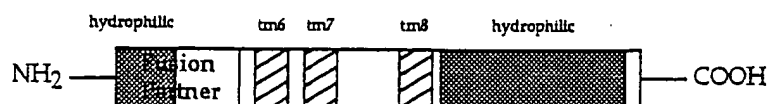


FIGURE 3

092225-00001

PUTATIVE MANNOSYL TRANSFERASE 5'-FUSION TRANSCRIPT

OGTACAATGTGAAGAAAGTCTTGTACCTTTOGCTTTOCGOCATAATGGCAGGGGCATCCAGTGGTTCAAGGTTACAATA

AGCTGTGATCGTGCCACTGCATTCTAOCCTGGGATGACAGAGTGGGAOCCTGTGOCACAGAGTGAGAACCTGTCTCAAAAA

M T E W D P V P Q S E T L S Q K

AAAAAACTATGTAAATCCAAGGAGAAGACTTCAOCCTGTATTGTACCTCTCCAAGTTCTGGAAAGTCGATGGAGGGTTTAC

K K L C K S K E T T S P V L Y L S K F W K V D G G F T

CAGAACTTCAATCTATCCAGAACTGAGTTTTGTTTTATGGTGTGTGCCAGTTCAGAAATTTAGGOCACCCGATTGGCTTA

Q N F N L S R T E F C L W C V P

CCTTGGCTCCAATGTATATTTGGTTTATAATTTCTTCATCCAGCCTCACAAAGAGGAGAGATTTCTTTTCCCTGTGTAT
CCACTTATATGTCTCTGTGGCGCTGTGGCTCTCTCTGCACTTCAGAAATGTTACCACTTTGTGTTTCAAOGATATOGCT
GGAGCACTATACTGTGACATOGAATTGGCTGGCATTAGGAACTGTCTTCTGTTTGGGCTCTTGTCAATTTCTOGCTCTG
TGGCACTGTTTCAAGGATATCAOGGGCCCCCTTGATTTGTATCCAGAATTTTACCGAATTGCTACAGACCCAAOCATCCAC
ACTGTCCCAGAAGGCAGAOCTGTGAATGTCTGTGTGGGAAAAGAGTGGTATOGATTTCCAGCAGCTTCTTCTTCTGA
CAATTGGCAGCTTCAGTTTCAATCCATCAGAGTTCAGAGGTCAGTTAOCAAAACCTTTTGCAGAAGGAOCCTCTGGCCACCC
GGATTGTTCCCTACTGACATGAATGACCAGAATCAGAAGAGOCATCCAGATATATTGATATCAGTAAATGCCATTATTTAG
TGGATTTGGACACCATGAGAGAAACACCCCGGGAGOCAAAATATTATOCATAAAGAAGAATGGATCAGCTTGGCCTAT
AGAOCATTOCTTGATGCTTCTAGATCTTCAAAGCTGCTGCGGGCATTCTATGTCCOCTTCTGTGATCAGTATACAGT
GTAOGTAACTACAOCATCTCAAAACCCCGGAAAGCAAAGCAAATCAGGAAGAAAAGTGGAGGTTAGCAACACAOCTGTG
GCCCCAAAGGACAACCATCTTGTTAACTATTGATTCAGTGAOCTGACTOCTGCAAGTCATCGOCTGTAACATTTGTAA
AAAGGTCTTCTGACATGAAAAAAAAAAAA

FIGURE 4

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Putative Fusion protein chr 11/9

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                NcoI
                ~~~~~
1      Met AlaSerArg GlyAlaArg GlnArgLeuLys GlySerGly·
      A TGGCTAGTCG AGGGGCTCGG CAGCGCCTGA AGGGCAGCGG
      T ACCGATCAGC TCCCCGAGCC GTCGCGGACT TCCCGTCGCC
                ~~~~~
51     ·AlaSerSer GlyAspThrAla ProAlaAla AspLysLeu ArgGluLeuLeu·
      GGCCAGCAGT GGGGATACGG CCCC GGCTGC GGACAAGCTG CGGGAGCTGC
      CCGGTCGTCA CCCCTATGCC GGGGCCGACG CCTGTTCGAC GCCCTCGACG
      ~~~~~
101    ·LGlySerArg GluAlaGly GlyAlaGluHis ArgThrGlu LeuSerGly
      TGGGCAGCCG AGAGGCGGGC GGCGCGGAGC ACCGGACCGA GTTATCTGGG
      ACCCGTCGGC TCTCCGCCCCG CCGCGCCTCG TGGCCTGGCT CAATAGACCC
      ~~~~~
151    AsnLysAlaGly GlnValTrp AlaProGlu GlySerThrAla PheLysCys·
      AACAAAGCAG GACAAGTCTG GGCACCTGAA GGATCTACTG CTTTCAAGTG
      TTGTTTCGTC CTGTTTCAGAC CCGTGGACTT CCTAGATGAC GAAAGTTCAC
      ~~~~~
201    ·LeuLeuSer AlaArgLeuCys AlaAlaLeu LeuSerAsn IleSerAspCys·
      TCTGCTTTCA GCAAGGTTAT GTGCTGCTCT CCTGAGCAAC ATCTCTGACT
      AGACGAAAGT CGTTCCAATA CACGACGAGA GGACTCGTTG TAGAGACTGA
      ~~~~~
251    ·CAspGluThr PheAsnTyr TrpGluProThr HisTyrLeu IleTyrGly
      GTGATGAAAC ATTCAACTAC TGGGAGCCAA CACACTACCT CATCTATGGG
      CACTACTTTG TAAGTTGATG ACCCTCGGTT GTGTGATGGA GTAGATACCC
      ~~~~~
301    GluGlyPheGln ThrTrpGlu TyrSerPro AlaTyrAlaIle ArgSerTyr·
      GAAGGGTTTC AGACTTGGGA ATATTCCCCA GCATATGCCA TTCGCTCCTA
      CTTCCCAAAG TCTGAACCCT TATAAGGGGT CGTATACGGT AAGCGAGGAT
      ~~~~~
                EcoRI
                ~~~~~
351    ·AlaTyrLeu LeuLeuHisAla TrpProAla AlaPheHis AlaArgIleLeu·
      TGCTTACCTG TTGCTTCATG CCTGGCCAGC TGCATTTTCAT GCAAGAATTC
      ACGAATGGAC AACGAAGTAC GGACCGGTCG ACGTAAAGTA CGTTCTTAAG
      ~~~~~
401    ·LGlnThrAsn LysIleLeu ValPheTyrPhe LeuArgCys LeuLeuAla
      TACAACTAA TAAGATTCTT GTGTTTTACT TTTTGCGATG TCTTCTGGCT
      ATGTTTGATT ATTCTAAGAA CACAAAATGA AAAACGCTAC AGAAGACCGA
      ~~~~~
451    PheValSerCys IleCysGlu LeuTyrPhe TyrLysAlaVal CysLysLys·
      TTTGTGAGCT GTATTTGTGA ACTTTACTTT TACAAGGCTG TGTGCAAGAA
      AAACACTCGA CATAAACT TGAATGAAA ATGTTCCGAC ACACGTTCTT
      ~~~~~
501    ·PheGlyLeu HisValSerArg MetMetLeu AlaPheLeu ValLeuSerThr·
      GTTTGGGTTG CACGTGAGTC GAATGATGCT AGCCTTCTTG GTTCTCAGCA
      CAAACCCAAC GTGCACTCAG CTTACTACGA TCGGAAGAAC CAAGAGTCGT

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FIGURE 5

FIGURE 5


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~~~~~
551  •TGlyMetPhe CysSerSer SerAlaPheLeu ProSerSer PheCysMet
    CTGGCATGTT TTGCTCATCA TCAGCATTCC TTCCTAGTAG CTTCTGTATG
    GACCGTACAA AACGAGTAGT AGTCGTAAGG AAGGATCATC GAAGACATAC
    ~~~~~
601  TyrThrThrLeu IleAlaMet ThrGlyTrp TyrMetAspLys ThrSerIle
    TACACTACGT TGATAGCCAT GACTGGATGG TATATGGACA AGACTTCCAT
    ATGTGATGCA ACTATCGGTA CTGACCTACC ATATACCTGT TCTGAAGGTA
    ~~~~~
651  •AlaValLeu GlyValAlaAla GlyAlaIle LeuGlyTrp ProPheSerAla
    TGCTGTGCTG GGAGTAGCAG CTGGGGCTAT CTTAGGCTGG CCATTCAAGT
    ACGACACGAC CCTCATCGTC GACCCCGATA GAATCCGACC GGTAAGTCAC
    ~~~~~
701  •AAlaLeuGly LeuProIle AlaPheAspLeu LeuValMet LysHisArg
    CAGCTCTTGG TTTACCCATT GCCTTTGATT TGCTGGTCAT GAAACACAGG
    GTCGAGAACC AAATGGGTAA CGGAAACTAA ACGACCAGTA CTTTGTGTCC
    ~~~~~
751  TrpLysSerPhe PheHisTrp SerLeuMet AlaLeuIleLeu PheLeuVal
    TGGAAGAGTT TCTTTCATTG GTCGCTGATG GCCCTCATAC TATTTCTGGT
    ACCTTCTCAA AGAAAGTAAC CAGCGACTAC CGGGAGTATG ATAAAGACCA
    801  •ProValVal ValIleAspSer TyrTyrTyr GlyLysLeu ValIleAlaPro
    GCCTGTGGTG GTCATTGACA GCTACTATTA TGGGAAGTTG GTGATTGCAC
    CGGACACCAC CAGTAACGTG CGATGATAAT ACCCTTCAAC CACTAACGTG
    851  •PLeuAsnIle ValLeuTyr AsnValPheThr ProHisGly ProAspLeu
    CACTCAACAT TGTTTTGTAT AATGTCTTTA CTCCTCATGG ACCTGATCTT
    GTGAGTTGTA ACAAACATA TTACAGAAAT GAGGAGTACC TGGACTAGAA
    TyrGlyThrGlu ProTrpTyr PheTyrLeu IleAsnGlyPhe LeuAsnPhe
    901  TATGGTACAG AACCTGGTA TTTCTATTTA ATTAATGGAT TTCTGAATTT
    ATACCATGTC TTGGGACCAT AAAGATAAAT TAATTACCTA AAGACTTAAA
    •AsnValAla PheAlaLeuAla LeuLeuVal LeuProLeu ThrSerLeuMet
    951  CAATGTAGCC TTTGCTTTGG CTCTCCTAGT CCTACCACTG ACTTCTCTTA
    GTTACATCGG AAACGAAACC GAGAGGATCA GGATGGTGAC TGAAGAGAAT
    PstI
    ~~~~~
1001 •MgluTyrLeu LeuGlnArg PheHis
    TGGAATACCT GCTGCAGAGA TTTCATG
    ACCTTATGGA CGACGTCTCT AAAGTAC

```

FIGURE 5

Putative fusion protein 9/11

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1   CGTACAATGT GAAGAAAGTC CTTGTACCCT TCGCCTTCCG CCATAATGGC
   GCATGTTACA CTTCTTTCAG GAACATGGGA AGCGGAAGGC GGTATTACCG
51  AGGGGCAATC CAGTGGTTCA AGGTTACAAT AAGCTGTGAT CGTGCCACTG
   TCCCCGTTAG GTCACCAAGT TCCAATGTTA TTCGACACTA GCACGGTGAC
       MetThrGlu TrpAspPro ValProGln SerGluThrLeu·
       ~~~~~

101  CATTCTACCT GGGATGACAG AGTGGGACCC TGTGCCACAG AGTGAGACCC
   GTAAGATGGA CCCTACTGTC TCACCCTGGG ACACGGTGTC TCACTCTGGG
   ·LSerGlnLys LysLysLeu CysLysSerLys GluThrThr SerProVal
   ~~~~~

151  TGTCTCAAAA AAAAAAATA TGTAATCCA AGGAGACGAC TTCACCTGTA
   ACAGAGTTTT TTTTTTTGAT ACATTTAGGT TCCTCTGCTG AAGTGGACAT
   LeuTyrLeuSer LysPheTrp LysValAsp GlyGlyPheThr GlnAsnPhe·
   ~~~~~

201  TTGTACCTCT CCAAGTTCTG GAAAGTCGAT GGAGGGTTTA CTCAGAACTT
   AACATGGAGA GGTTCAAGAC CTTTCAGCTA CCTCCCAAAT GAGTCTTGAA
   ·AsnLeuSer ArgThrGluPhe CysLeuTrp CysValPro GlnAsnLeu·
   ~~~~~

251  CAATCTATCC AGAACTGAGT TTTGTTTATG GTGTGTGCCA GTTCAGAATT
   GTTAGATAGG TCTTGACTCA AAACAAATAC CACACACGGT CAAGTCTTAA
   ·LGlyHisPro TyrTrpLeu ThrLeuAlaPro MetTyrIle TrpPheIle
   ~~~~~

301  TAGGCCACCC GTATTGGCTT ACCTTGGCTC CAATGTATAT TTGGTTTATA
   ATCCGGTGGG CATAACCGAA TGAACCGAG GTTACATATA AACCAAATAT
   ~~~~~
   IlePhePheIle GlnProHis LysGluGlu ArgPheLeuPhe ProValTyr·
   ~~~~~

351  ATTTTCTTCA TCCAGCCTCA CAAAGAGGAG AGATTTCTTT TCCCTGTGTA
   TAAAAGAAGT AGGTCGGAGT GTTCTCCTC TCTAAAGAAA AGGGACACAT
   ~~~~~
   ·ProLeuIle CysLeuCysGly AlaValAla LeuSerAla LeuGlnLysCys·
   ~~~~~

401  TCCACTTATA TGTCTCTGTG GCGCTGTGGC TCTCTCTGCA CTTCAGAAAT
   AGGTGAATAT ACAGAGACAC CGCGACACCG AGAGAGACGT GAAGTCTTTA
   ~~~~~
   ·CTyrHisPhe ValPheGln ArgTyrArgLeu GluHisTyr ThrValThr
   ~~~~~

451  GTTACCACTT TGTGTTTCAA CGATATCGCC TGGAGCACTA TACTGTGACA
   CAATGGTGAA ACACAAAGTT GCTATAGCGG ACCTCGTGAT ATGACACTGT
   ~~~~~
   SerAsnTrpLeu AlaLeuGly ThrValPhe LeuPheGlyLeu LeuSerPhe·
   ~~~~~

501  TCGAATTGGC TGGCATTAGG AACTGTCTTC CTGTTTGGGC TCTTGTCATT

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FIGURE 6

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AGCTTAACCG ACCGTAATCC TTGACAGAAG GACAAACCCG AGAACAGTAA
~~~~~
·SerArgSer ValAlaLeuPhe ArgGlyTyr HisGlyPro LeuAspLeuTyr·
~~~~~
551 TTCTCGCTCT GTGGCACTGT TCAGAGGATA TCACGGGCCC CTTGATTTGT
AAGAGCGAGA CACCGTGACA AGTCTCCTAT AGTGCCCGGG GAACTAAACA
~~~~~
·TProGluPhe TyrArgIle AlaThrAspPro ThrIleHis ThrValPro
~~~~~
601 ATCCAGAATT TTACCGAATT GCTACAGACC CAACCATCCA CACTGTCCCA
TAGGTCTTAA AATGGCTTAA CGATGTCTGG GTTGGTAGGT GTGACAGGGT
Clai
~~~~~
GluGlyArgPro ValAsnVal CysValGly LysGluTrpTyr ArgPhePro·
~~~~~
651 GAAGGCAGAC CTGTGAATGT CTGTGTGGGA AAAGAGTGGT ATCGATTTCC
CTTCCGTCTG GACACTTACA GACACACCCT TTTCTACCA TAGCTAAAGG
·SerSerPhe LeuLeuProAsp AsnTrpGln LeuGlnPhe IleProSerGlu·
~~~~~
701 CAGCAGCTTC CTTCTTCCTG ACAATTGGCA GCTTCAGTTC ATTCCATCAG
GTCGTCAAG GAAGAAGGAC TGTTAACCGT CGAAGTCAAG TAAGGTAGTC
·GPheArgGly GlnLeuPro LysProPheAla GluGlyPro LeuAlaThr
~~~~~
751 AGTTCAGAGG TCAGTTACCA AAACCTTTG CAGAAGGACC TCTGGCCACC
TCAAGTCTCC AGTCAATGGT TTTGGAAAAC GTCTTCCTGG AGACCGGTGG
ArgIleValPro ThrAspMet AsnAspGln AsnLeuGluGlu ProSerArg·
~~~~~
801 CGGATTGTTC CTA CTGACAT GAATGACCAG AATCTAGAAG AGCCATCCAG
GCCTAACAAG GATGACTGTA CTTACTGGTC TTAGATCTTC TCGGTAGGTC
·TyrIleAsp IleSerLysCys HisTyrLeu ValAspLeu AspThrMetArg·
~~~~~
851 ATATATTGAT ATCAGTAAAT GCCATTATTT AGTGGATTTG GACACCATGA
TATATAACTA TAGTCATTTA CGGTAATAAA TCACCTAAAC CTGTGGTACT
SmaI
~~~~~
XmaI
~~~~~
AvaI
~~~~~
·AGluThrPro ArgGluPro LysTyrSerSer AsnLysGlu GluTrpIle
~~~~~
901 GAGAAACACC CCGGGAGCCA AAATATTCAT CCAATAAAGA AGAATGGATC
CTCTTTGTGG GGCCCTCGGT TTTATAAGTA GGTTATTTCT TCTTACCTAG
SerLeuAlaTyr ArgProPhe LeuAspAla SerArgSerSer LysLeuLeu·
~~~~~
951 AGCTTGGCCT ATAGACCATT CCTTGATGCT TCTAGATCTT CAAAGCTGCT
TCGAACCGGA TATCTGGTAA GGAACACGA AGATCTAGAA GTTTCGACGA
·ArgAlaPhe TyrValProPhe LeuSerAsp GlnTyrThr ValTyrValAsn·
~~~~~
1001 GCGGGCATTG TATGTCCCCT TCCTGTCAGA TCAGTATACA GTGTACGTAA
CGCCCGTAAG ATACAGGGGA AGGACAGTCT AGTCATATGT CACATGCATT
·ATyrThrIle LeuLysPro ArgLysAlaLys GlnIleArg LysLysSer

```

FIGURE 6

092225-00201

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~~~~~  
1051 ACTACACCAT CCTCAAACCC CGGAAAGCAA AGCAAATCAG GAAGAAAAGT  
      TGATGTGGTA GGAGTTTGGG GCCTTTCGTT TCGTTTAGTC CTTCTTTTCA  
      GlyGly  
      ~~~~~  
1101 GGAGGTTAGC AACACACCTG TGGCCCCAAA GGACAACCAT CTTGTTAACT  
      CCTCCAATCG TTGTGTGGAC ACCGGGGGTTT CCTGTTGGTA GAACAATTGA  
1151 ATTGATTCCA GTGACCTGAC TCCCTGCAAG TCATCGCCTG TAACATTTGT  
      TAACTAAGGT CACTGGACTG AGGGACGTTT AGTAGCGGAC ATTGTAAACA  
1201 AATAAAGGTC TTCTGACATG AAAAA  
      TTATTTCCAG AAGACTGTAC TTTTT
```

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FIGURE 6

Chromosome 9 est (gene) involved in fusion:

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1      AGCGGGTGGG CGCGAGTCGG CCTCCCGCGG TGCCGCCGCA GCGTGGCGCG
      TCGCCACCCC GCGCTCAGCC GGAGGGCGCC ACGGCGGCGT CGCACC GCGC
51     GAGAGGCAGG GGCATCCAGT GGTTC AAGGT TACAATAAGC TGTGATCGTG
      CTCTCCGTCC CCGTAGGTCA CCAAGTTCCA ATGTTATTCG AACTAGCAC
                                           Glu.
                                           ~~~
101    CCACTGCATT CTACCTGGGA TGACAGAGTG GGACCCTGTG CCACAGAGTG
      GGTGACGTAA GATGGACCTT ACTGTCTCAC CCTGGGACAC GGTGTCTCAC
      ·GThrLeuSer GlnLysLys LysLysLeuCys LysSerLys LysLysArg
      ~~~~~
151    AGACCCTGTC TCAAAAAAAAA AAAAAACTAT GTAAATCCAA GAAAAAAAAAGA
      TCTGGGACAG AGTTTTTTTTT TTTTGTGATA CATTTAGGTT CTTTTTTTCT
      LysGlnLeuLeu TrpProPhe AlaSerHis ProGluArgVal SerIleGly.
      ~~~~~
201    AAACAGCTCC TGTGGCCTTT TGCCTCTCAT CCAGAAAGGG TATCCATTGG
      TTTGTGAGG ACACCGGAAA ACGGAGAGTA GGTCTTCC C ATAGGTAACC
      ·LeuSerAsn IleSerSerSer CysGlnAla ThrAsnGly AspAspProPro.
      ~~~~~
251    CCTTTCTAAT ATCTCTTCAT CCTGTCAGGC CACAAATGGA GACGACCCAC
      GGAAAGATTA TAGAGAAGTA GGACAGTCCG GTGTTTACCT CTGCTGGGTG
      ·PValTrpTyr LeuSerLys PheTrpLysVal AspGlyGly PheThrGln
      ~~~~~
301    CTGTATGGTA CCTCTCCAAG TTCTGGAAAG TCGATGGAGG GTTTACTCAG
      GACATACCAT GGAGAGGTTC AAGACCTTTC AGCTACCTCC CAAATGAGTC
      AsnPheAsnLeu SerArgThr GluPheGly LysTrpCysVal ProGlyArg.
      ~~~~~
351    AACTTCAATC TATCCAGAAC TGAGTTTGGT AAATGGTGTG TGCCAGGCAG
      TTGAAGTTAG ATAGGTCTTG ACTCAAACCA TTTACCACAC ACGGTCCGTC
                                           EcoRI
                                           ~~~~~
      ·GlyLeuAsn SerSerAlaTyr HisTrpAla GluValThr GlyIleGlnGlu.
      ~~~~~
401    GGGATTAAAC AGTAGTGCAT ATCACTGGGC TGAAGTGACA GGAATTCAAG
      CCCTAATTTG TCATCACGTA TAGTGACCCG ACTTCACTGT CCTTAAGTTC
      ·GGlnAsnAla SerThrPro ProValSerLeu SerCysLeu PheLeuLeu
451    AACAGAATGC ATCCACTCCT CCAGTCTCAT TAAGCTGCCT CTTTCTACTG
      TTGTCTTACG TAGGTGAGGA GGTCAGAGTA ATTCGACGGA GAAAGATGAC
      LysTrpArgTrp GlyPheGln AspThrSer GlnProThrGly ThrThrGly.
501    AAATGGCGAT GGGGATTCCA GGACACCTCT CAACCTACAG GAACCACTGG
      TTTACCGCTA CCCCTAAGGT CCTGTGGAGA GTTGGATGTC CTTGGTGACC
      ·Ser
551    ATCTAA
      TAGATT

```

FIGURE 7

092225-030201

Human (SEQ ID NO: 2) (100%)

S. cerevisiae (ALG9) (SEQ ID NO:11) (33.1%)

Arabidopsis (SEQ ID NO: 12) (31.2 %)

C. elegans (SEQ ID NO: 13) (33.1%)

FIGURE 8

D. melanogaster (SEQ ID NO: 14) (40.6%)

mappaarary iankadnqil skkppkrpgl ngnnktkeat pagkkkdkda kkrnqptsgg
qekglpnpim psvqtafktf vsarlcsaiw ayiadcdetf nyweplhyii nghglqtwey
spqfglrst ylllqgvpgy fyqklfnpsp ilifymvrcm lgfgcavmer ymyksicqef
gihigrwlwli fqlfsvgmfv sstallpssf smyfgcaala awwqqnycfa ifltaisall
gwpfaaligi plvlemlrrq rdwktfvqwt lisgatvaip miaidtsyfg klrtaplniv
wynvftshgp nifgteplsy yingflnfn iiwllalqlp imlvidyliv pakskstlnf
phyislaply lwllvffaqp hkeerflfpi yplislcgai tvdvyrgriff rmksvfvkik
agvhyldhsm fiailmvmts tllglsvrfa lyrnyhapmd lmlelnqfka tpqydpdviy
nvcigkdwhr ypgsffffpak nfrlrflkse frgmlpayyd eggnatkvvq pyfndlnqen
ehmyfdydrc dflvdfdegk ytalepnysk rskdwsvmks lpflipeksh kvlrafyvpf
ltdnhiqygd fnllkrktr ngr

S. pombe (SEQ ID NO: 15) (33.1%)

mpskaprksl svsvfwtfsl lavlrlltsas frviddcdev ynyweplhyl lygyglqtwe
yspeyairsw fyialhavpg flarglglsr lhfvyfirgv lacfsafcet nlilavarnf
nravalhlts vlfvnsqmw sstsfllpssf amnmvtlals aqlsppstkr tvkvvsfity
gavigwpfsa alsipfille lvdikgrfrh lfcwrfkaif vallitgici tvdslyfhyri
qfvaunivky nvlakdgrgp diygtepwyy yfanlsiqhn ivlwfamacg plvllaafn
winldsflldl ssvispfyiw lfifiiqphk eerfmypiyp vlclaaaigl dmslklmiqi
lssinetvrs kfpvrffvvc vyaiigclsi arilaiqnyn apmiiypais fletdnnvtt
nvcvgkewyr ypstfflpdn srlkfvksef dgilpgefve snstwnnreg yyqipehmne
fnneeptryt slescdflid lefdhskatv nepiysksdg wipvmvypfi dtkqtpfmgr
afavpfiepk wgyeilvkk pvkidfsnlr raskqqa

The diagram illustrates the RT-PCR protocol for generating a fusion transcript. It begins with an mRNA template (3' end) and a fusion partner template (5' end). The process involves reverse transcription (RT) using dATP and TdT, with a GSP primer. The resulting cDNA ss is then amplified by PCR for 6 cycles, followed by PST-1 digestion and re-amplification for 6 cycles. The final product is a fusion transcript, which is then used for cDNA ds synthesis.

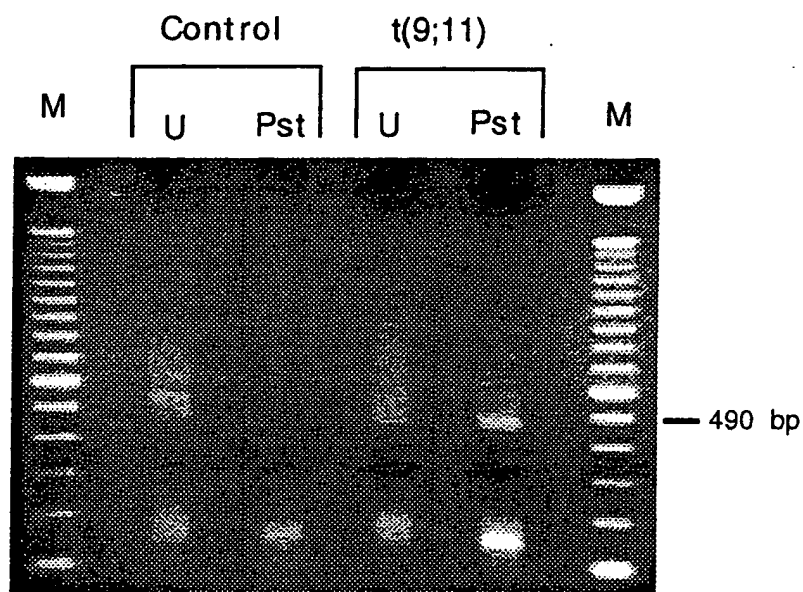


FIGURE 9

Figure 5 Expression Studies

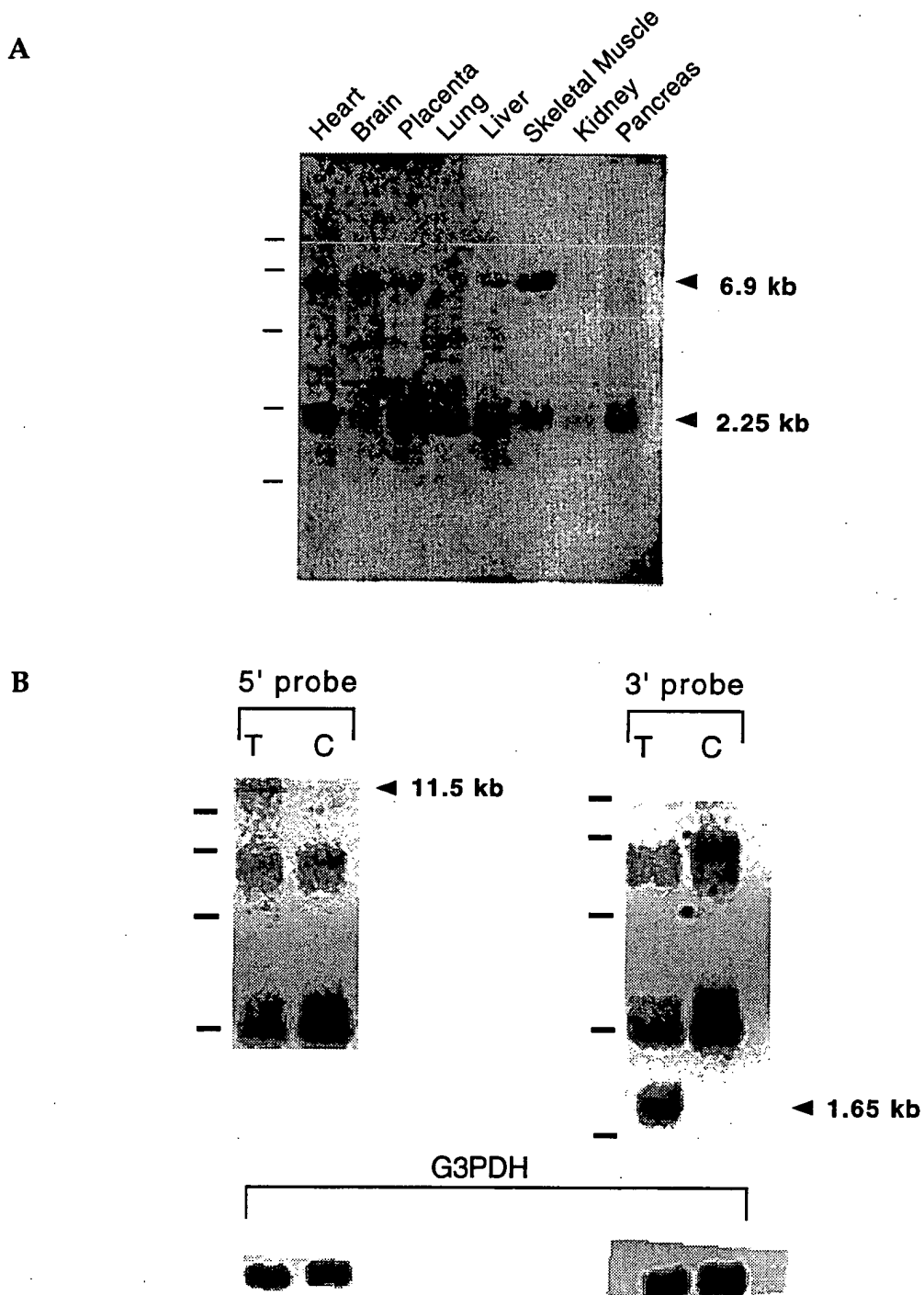


FIGURE 10